

WHAT IS CLAIMED IS:

1. A method for improving the reliability of physical measurements obtained from array hybridization studies performed
5 on an array having a large number of genomic samples, each composed of a small number of replicates insufficient for making precise and valid statistical inferences, comprising the step of estimating an error in measurement of a sample by averaging errors obtained when measuring at least one of the large number of
10 samples and a subset of the large number of samples, and utilizing the estimated sample error as a standard for accepting or rejecting the measurement of the respective sample.
2. The method of claim 1 wherein a physical measurement
15 quantity is determined based on the difference between statistically dependent quantities.
3. The method of claim 1 wherein a physical measurement quantity determined from an entire array population is used to
20 estimate discrete instances of that quantity for the small number of replicate samples within that population.
4. The method of claim 1 wherein the estimates of measurement error are used to plan, manage and control array
25 hybridization studies on the basis of (a) the probability of detecting a true difference of specified magnitude between physical measurements of a given number of replicates, or (b) the number of replicates required to detect a true difference of specified magnitude.
30
5. A method for improving the reliability and accuracy of physical measurements obtained from array hybridization studies performed
on an array having a large number of genomic samples, each composed
35 of a small number of replicates insufficient for making precise and valid statistical inferences, comprising the step of

detecting outlier values in the measurement of a sample by combining residuals of values obtained when measuring one of the large number of samples and a subset of the large number of samples.

5 6. The method of claim 5 wherein outliers are detected based on the deviation of their residual values from one of the mean, median and other measurement of the residual values.

7. The method of claim 5 wherein outliers are detected
10 manually based on characteristics, including skew and kurtosis, of the distribution of residual values.

8. The method of claim 5 wherein outliers are detected based on at least one of automatically and iteratively, with respect
15 to the characteristics, including skew and kurtosis, of the distribution of residual values.

9. A method for improving the accuracy of physical measurements obtained from array hybridization studies performed on
20 an array having a large number of genomic samples, each composed of a small number of replicates insufficient for estimating offset across arrays, the method comprising the step of averaging the differences between individual samples within one array and the average of the certain replicates across other arrays that include
25 said one array.

10. A method for improving the accuracy of physical measurements obtained from array hybridization studies performed on an array having a large number of genomic samples across two or more
30 conditions, each composed of a small number of replicates insufficient for estimating offset across arrays, wherein measurements obtained from certain replicates are correlated across conditions, the method comprising the step of averaging the differences between individual samples within one array and the
35 average of the certain replicates across other arrays that include said one array.

11. The method of any one of claims 5-10 wherein a physical measurement quantity is determined based on the difference between statistically dependent quantities.

5 12. The method of any one of claims 5-10 wherein a physical measurement quantity determined from an entire array population is used to estimate discrete instances of that quantity for the small number of replicate samples within that population.

10 13. The method of any one of claims 5-10 wherein the estimates of measurement error are used to plan, manage and control array hybridization studied on the basis of (a) the probability of detecting a true difference of specified magnitude between physical measurements; of a given number of replicates, or (b) the number of
15 replicates; required to detect a true difference of specified magnitude.

 14. The method of claim 10 used to evaluate physical measurements obtained from biological and chemical assays conducted
20 in one of substrates, substrates containing wells, and test tubes.

 15. The method of claim 11 used to evaluate physical measurements obtained from biological and chemical assays conducted in one of substrates, substrates containing wells, and test tubes.
25

 16. The method of claim 12 used to evaluate physical measurements obtained from biological and chemical assays conducted in one of substrates, substrates containing wells, and test tubes.

30 17. The method of claim 13 used to evaluate physical measurements obtained from biological and chemical assays conducted in one of substrates, substrates containing wells, and test tubes.